Grape Day
June 5, 2024

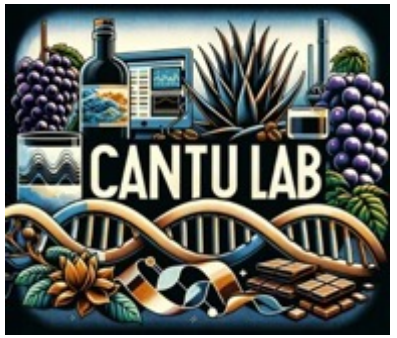
Wild grapes are a reservoir of genetic diversity for the future of viticulture

Dario Cantù

Professor and Louis P. Martini Endowed Chair

VITICULTURE & ENOLOGY
UNIVERSITY OF CALIFORNIA DAVIS

genome center



Functional grape genomics

Understand the genetic bases of viticulture traits

Vineyard phenotypes

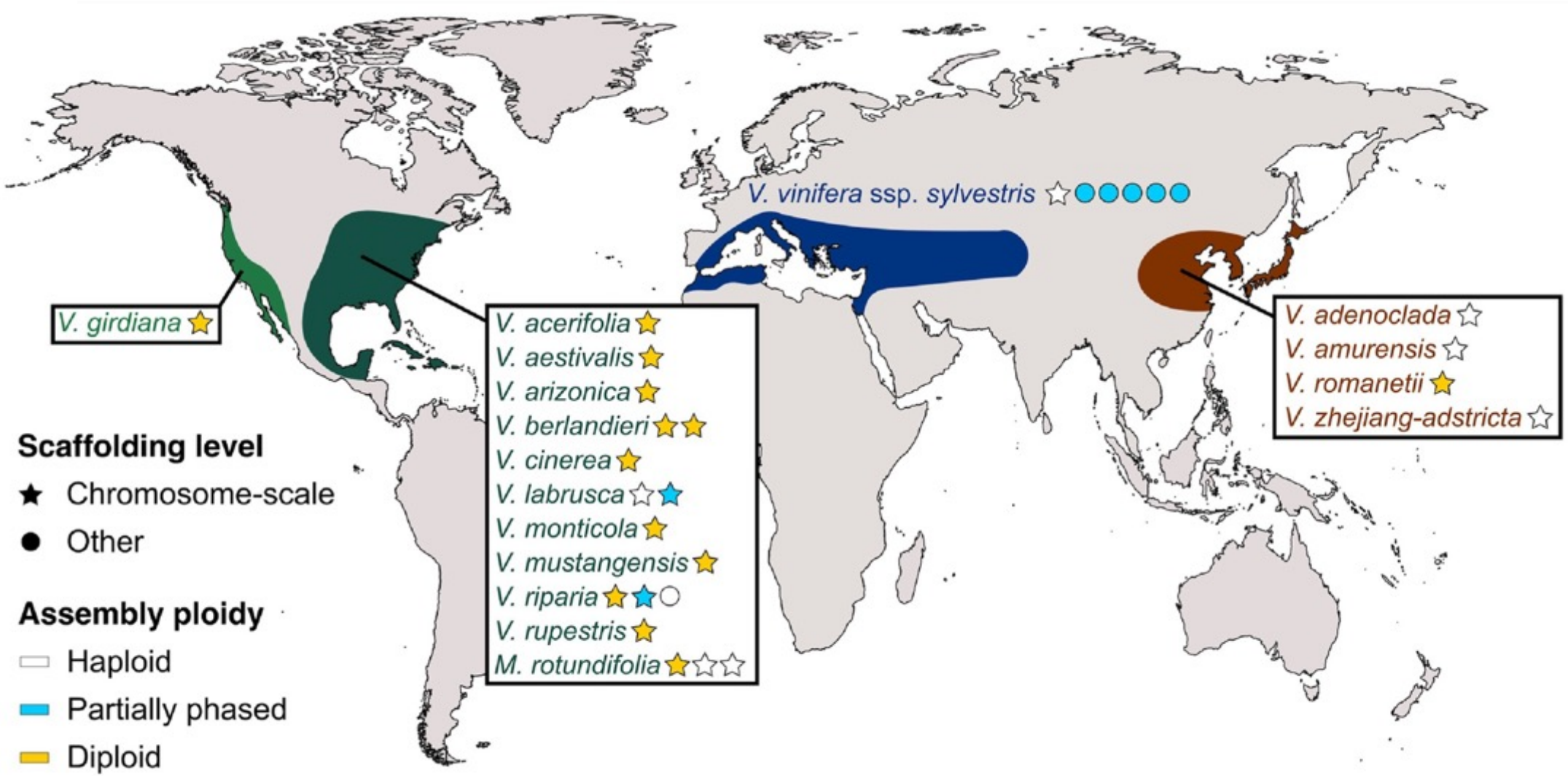
Grape genome

Incorporation of traits that improve sustainability, productivity, and resilience of grape production

Vitis species

- Approximately 60-70 species
- Native to temperate regions of the Northern Hemisphere in the Americas and Asia
- Evolved in a broad variety of environments
- Dioecious and interfertile
- Examples: *Vitis vinifera, Vitis rupestris*, *Vitis berlandieri*, *Vitis riparia, Vitis arizonica, Vitis piasezkii*

The dawn of wild grape genomics, genetics, and utilization

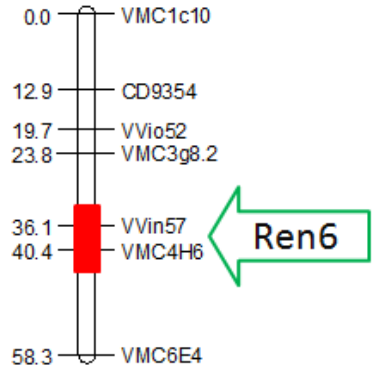


Cantu et al. 2024, Trends in Genetics

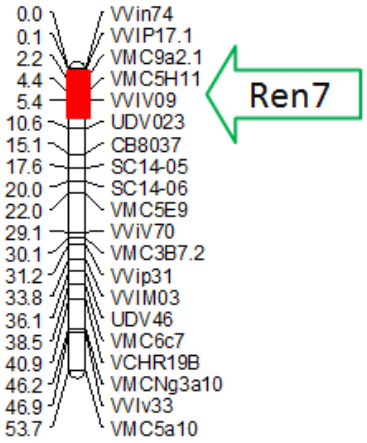
Genetic disease resistance to powdery mildew

Vitis piasezkii

Chromosome 9



Chromosome 19



Pap et al., 2016 BMC Plant Biol

Genetic disease resistance to powdery mildew

Ren2
V. cinerea x V. rupestris

Ren3
american sp. (`Regent`)

Ren5

Run1

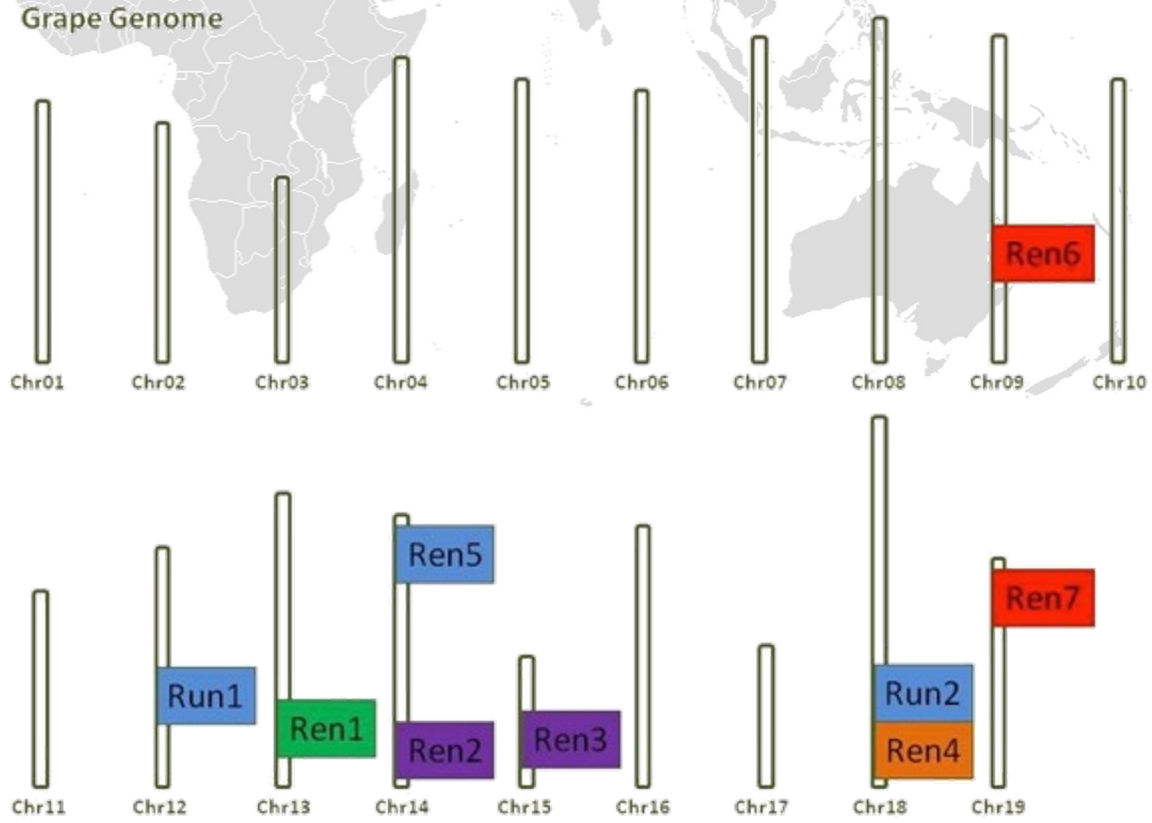
Run2
M. rotundundifoila

Ren1
V. sylvestris/vinifera

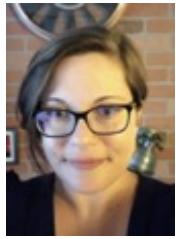
Ren4
V. romeneti

Ren6

Ren7
V. piazeskii




Manon Paineau


Mélanie Massonnet


Maria Sole Bonarota

VitisGen3: Developing Next Gen Tools for the Grape Research Community

Objective 1: Gene on the shelf

New knowledge of powdery mildew candidate gene function
Implement gene editing for disease resistance
Extend the life of resistant varieties

Objective 2: Tools in the toolbox

Advance computer vision phenotyping, AI, and DNA markers for US grape breeders nationwide.

Objective 3: Sticks in the ground

Reduced pesticide inputs using disease resistant spray programs (via field trial)
Develop new sustainable vineyard practices (via field trial)
New cultivars and enhanced breeding pipelines for regionally important traits and disease resistance (via participating breeding programs)

Objective 4: Grapes on the table

Learning how to communicate benefits of new varieties
Clear guidelines for marketing disease resistant varieties in different regional grape markets

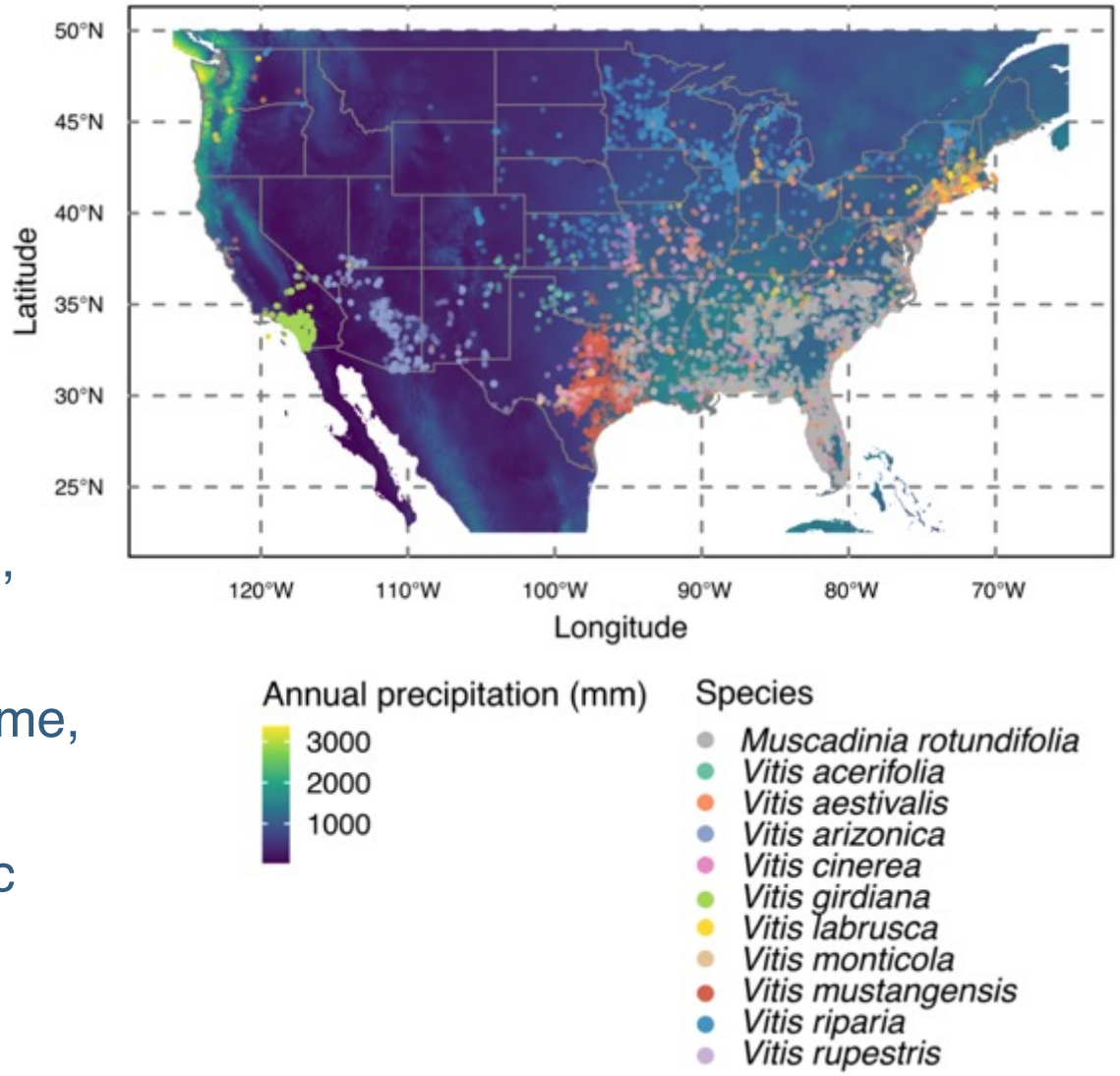
Award No. 2022-51181-38240

North American *Vitis* species

- About 30 species of wild *Vitis*
- Inhabit a wide range of environments
- Sources of tolerance/resistance for the domesticated cultivars
- Represent a large panel of desired agronomical traits:

  Biotic stress resistance (PD, nematodes, phylloxera)

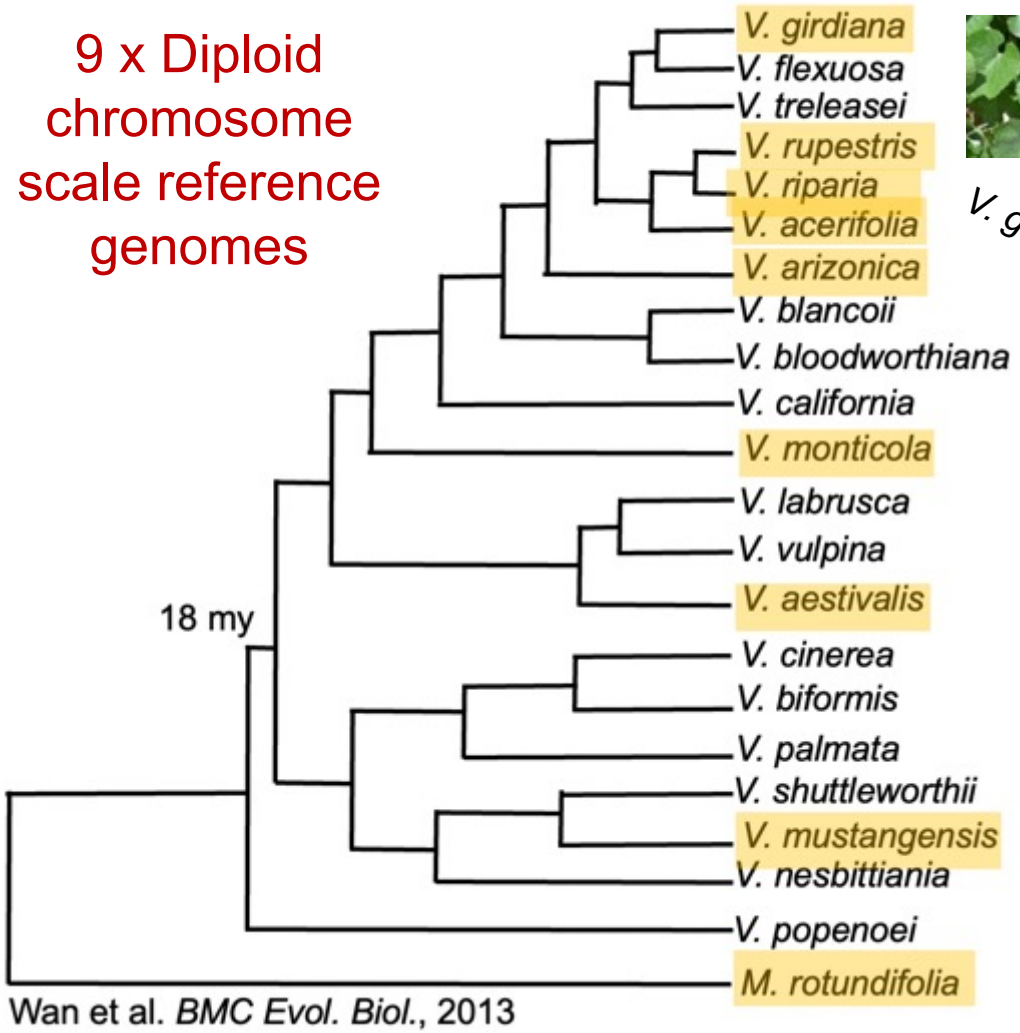
  Abiotic stress tolerance (Cl^- exclusion, lime, cold, drought)
- Dioecious and interfertile: source of genetic diversity



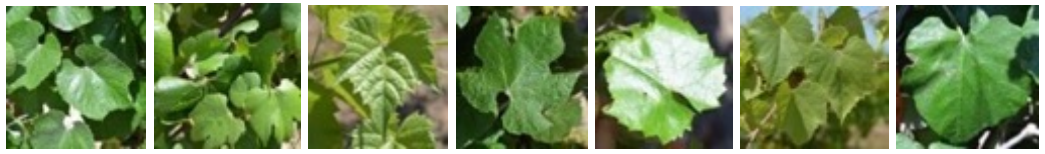
Cantu et al., 2024 *Trends in Genetics*

Evolution of genetic resistance to Pierce's disease and salt tolerance in Southwest *Vitis* spp.

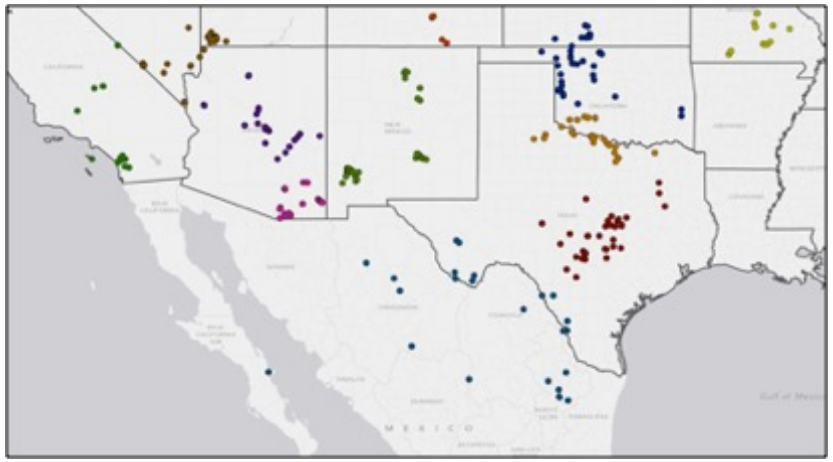
9 x Diploid chromosome scale reference genomes



Wan et al. *BMC Evol. Biol.*, 2013



V. girdiana *V. berlandieri* *V. acerifolia* *V. aestivalis* *V. monticola* *V. arizonica* *V. mustan.*

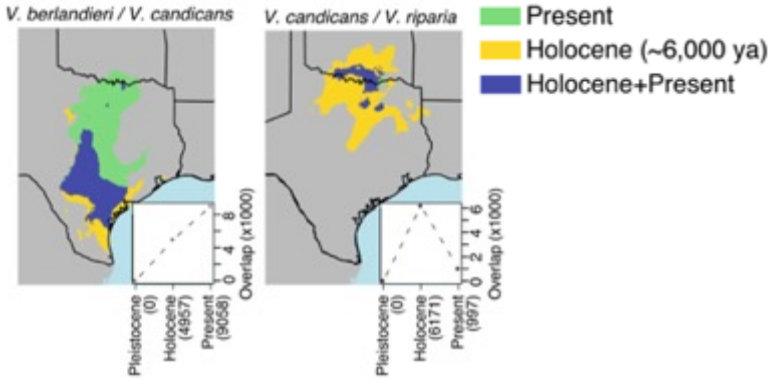


~1,000 WGS sequenced accessions

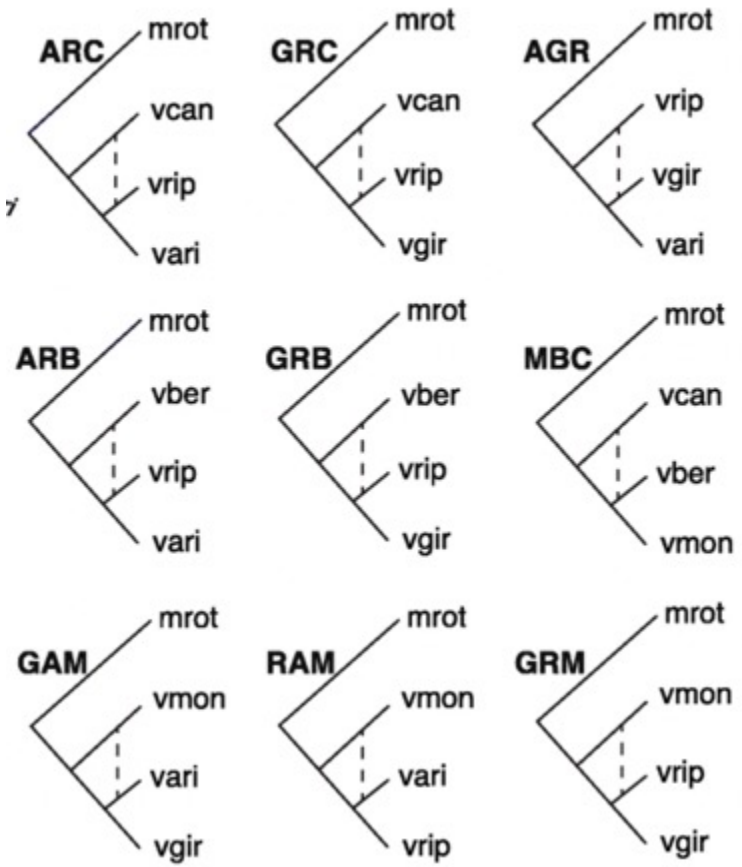
PD susceptibility and salt tolerance phenotyping

RESEARCH-PGR #1741627

Introgression among North American wild grapes (*Vitis*)



Introgression tests



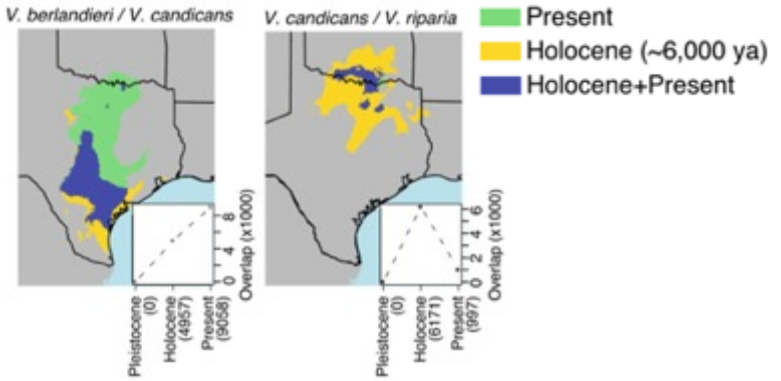
Putative introgressed regions (pIRs)

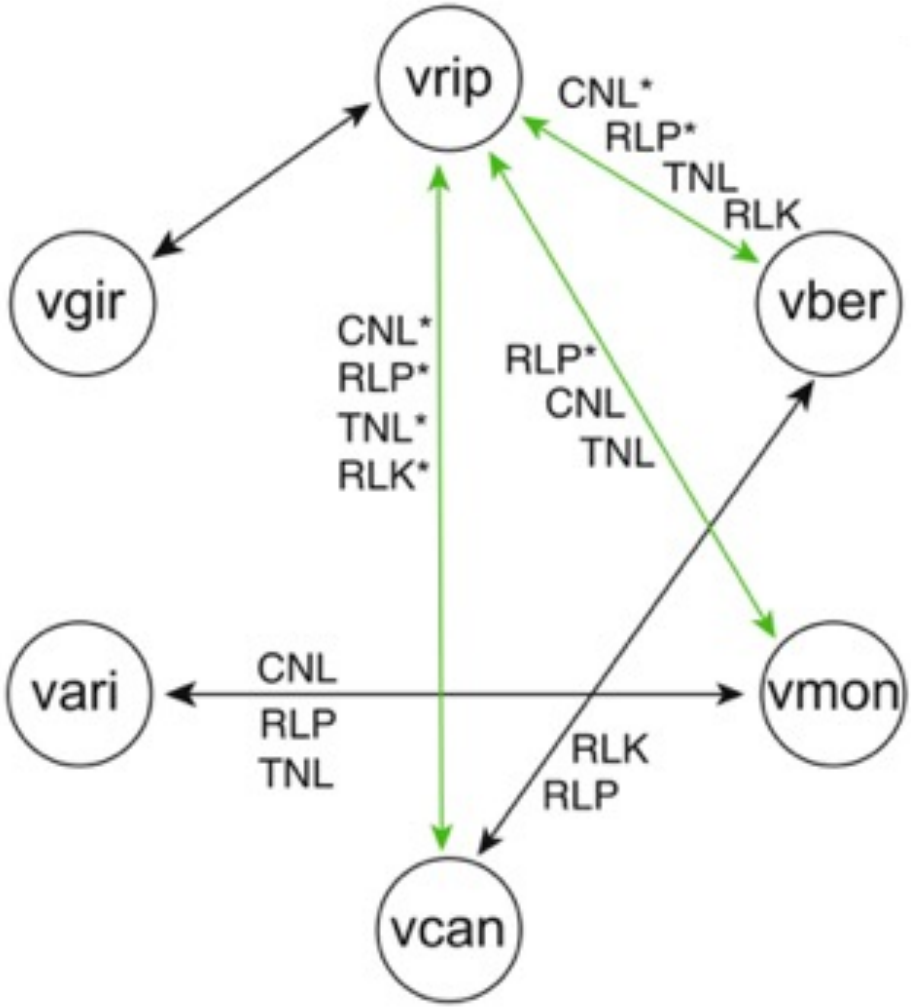
Trio[a]	P2	P3	f_4-ratio	Mean pIRs (Kb)[b]	No. genes
GAM	*arizonica*	*monticola*	8.03%	269.36	2282
RAM	*arizonica*	*monticola*	2.07%	210.44	597
MBC	*berlandieri*	*candicans*	3.24%	163.23	746
AGR	*girdiana*	*riparia*	3.32%	154.49	955
GRM	*riparia*	*monticola*	6.08%	270.68	1325
GRB	*riparia*	*berlandieri*	7.47%	233.29	1538
ARB	*riparia*	*berlandieri*	7.40%	200.07	1607
ARC	*riparia*	*candicans*	2.43%	226.25	480
GRC	*riparia*	*candicans*	2.30%	217.32	455

A: *V. arizonica*, B: *V. berlandieri*, C: *V. candicans*,
G: *V. girdiana*, M: *V. monticola*, and R: *V. riparia*

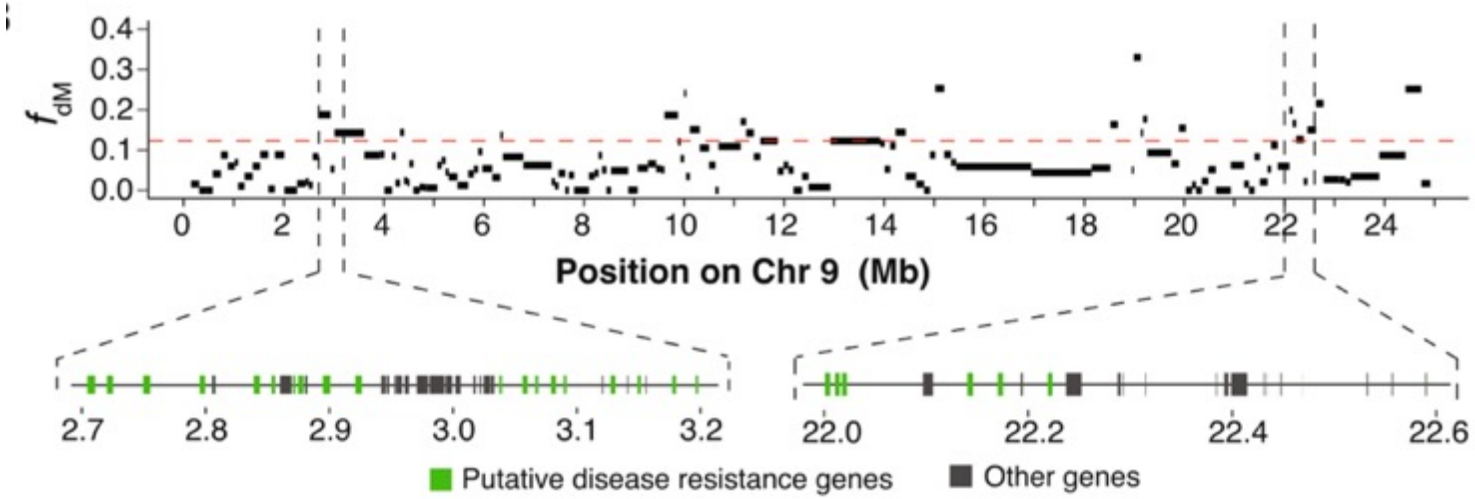
Morales-Cruz et al., 2021 *Genome Biology*

Introgression among North American wild grapes (*Vitis*)





Putative introgressed loci are enriched in disease resistance genes



Morales-Cruz et al., 2021 *Genome Biology*

Characterization of the genetic diversity of North American grape species

A super-pangenome of the North American wild grape species

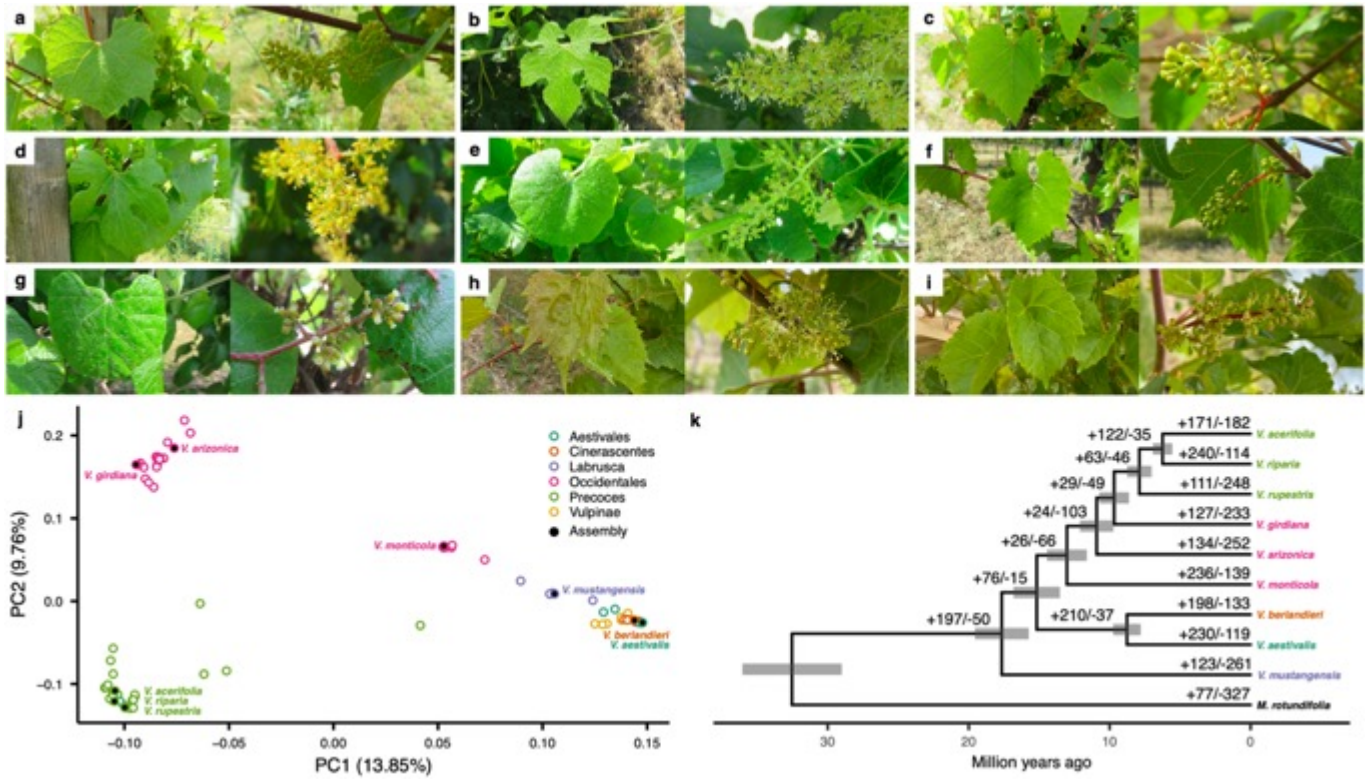
Noé Cochetel[1], Andrea Minio[1], Andrea Guarracino[2,3], Jadran F. Garcia[1], Rosa Figueroa-Balderas[1], Mélanie Massonnet[1], Takao Kasuga[4], Jason P. Londo[5], Erik Garrison[2], Brandon S. Gaut[6] and Dario Cantu[1,7*]

Cochetel *et al. Genome Biology* (2023) 24:290
https://doi.org/10.1186/s13059-023-03133-2

1 x super-pangenome =

9 x wild *Vitis* spp. diploid chromosome scale genomes +

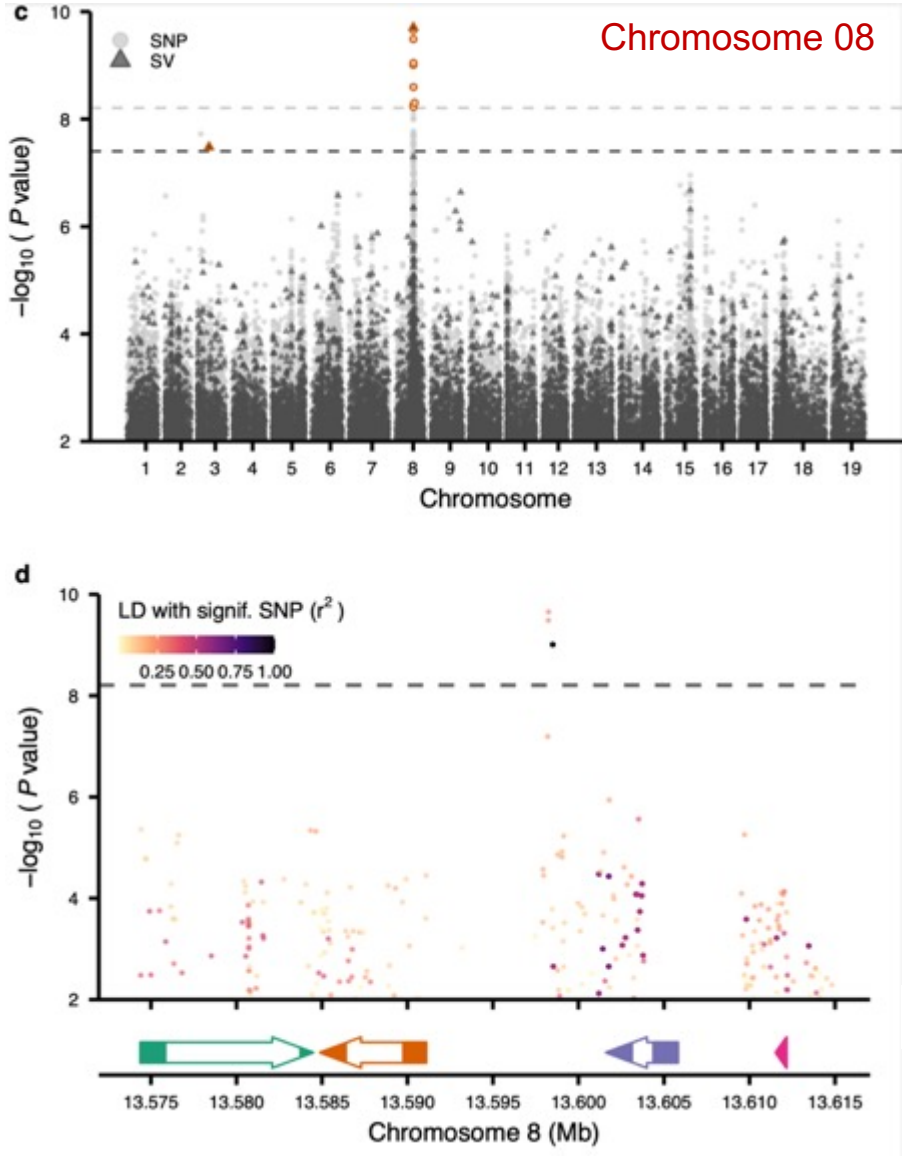
481 x whole genome sequences of wild *Vitis* spp. accessions

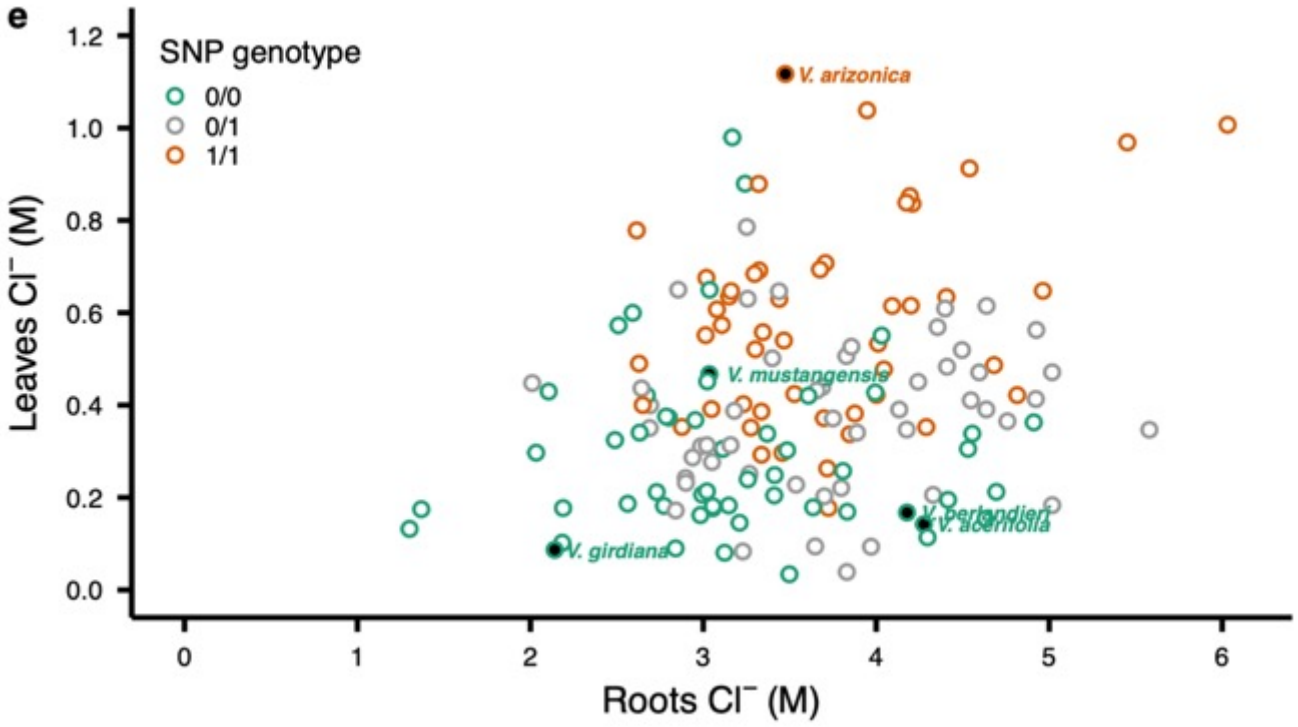


Cochetel et al., 2023 *Genome Biology*

Genetics of salt tolerance (Cl^- exclusion)

Leaves Cl^-





AGD6 CHX20 CHX20 histone H4 domain protein

CHX20 = cation/H+ exchanger 20

Cochetel et al., 2023 *Genome Biology*

Rootstock breeding for tolerance to boron toxicity (Diaz Garcia's lab)

0.5 ppm (C) 8.0 ppm

1103P

0.5 ppm (C) 8.0 ppm

SAZ4 (*V. arizonica*, Arizona)

0.5 ppm (C) 8.0 ppm

T03-15 (*V. rupestris*, Texas)

Breeding new varieties for PD resistance

Vitis arizonica

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New PD-Resistant Wine Grape Varieties Named and Released

Patents Filed for Walker-bred Cultivars Developed at UCD

by ***Ted Rieger***
December 03, 2019

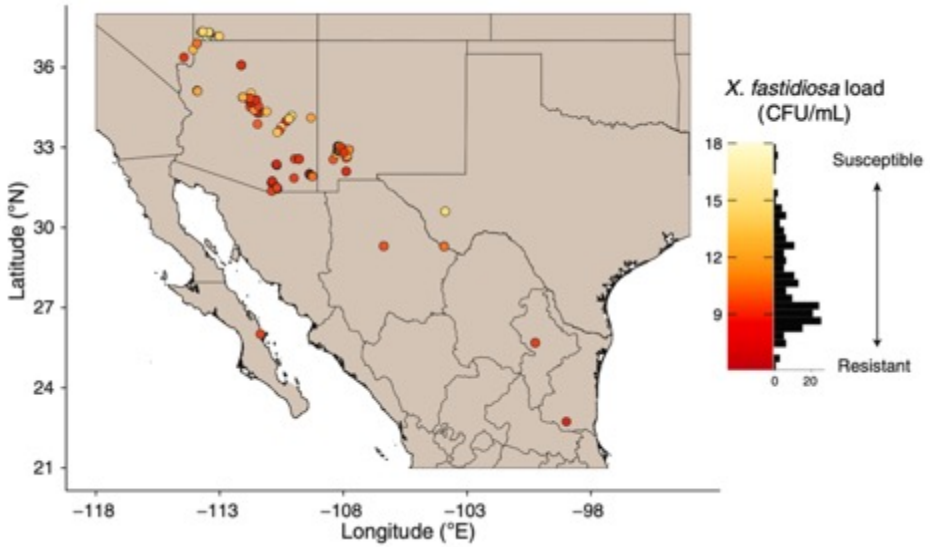
UCD viticulture professor and grape breeder Dr. Andy Walker developed the five PD-resistant wine grape varieties with research funding from the CDFA PD/GWSS Board. Photo: Ted Rieger

PD resistant varieties:

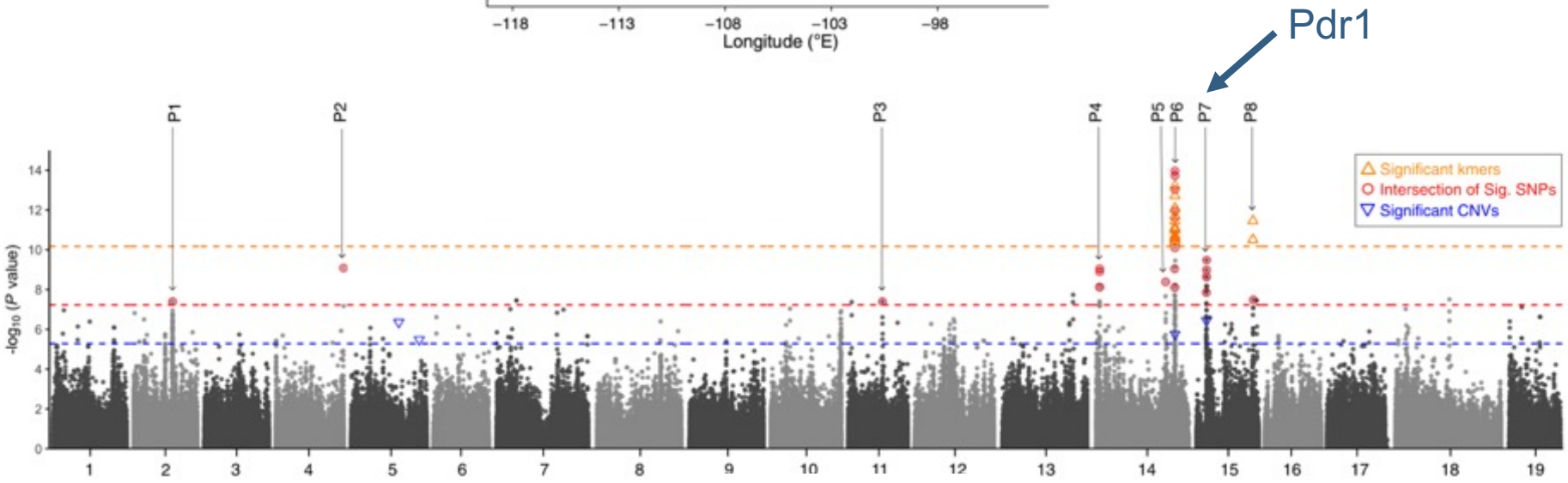
Camminare Noir
Paseante Noir
Errante Noir
Ambulo Blanc
Caminante Blanc

Multigenic resistance to PD in *Vitis arizonica*

Sampling and PD testing

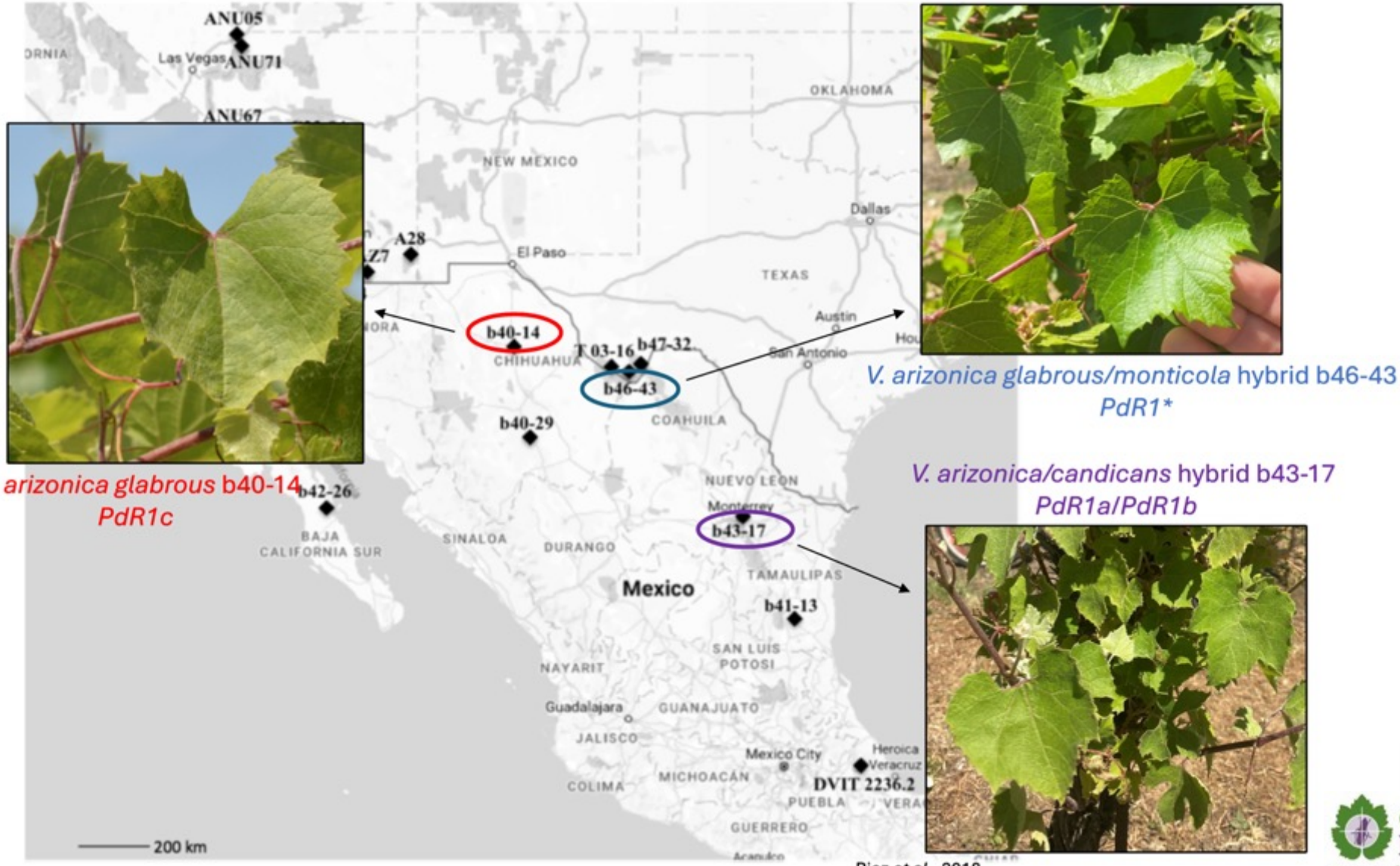


Genomic regions associated with PD resistance



Morales-Cruz et al., 2023 Comm Biol

Other forms of genetic resistance to PD?



Mirella Zaccheo

Riaz *et al.*, 2018

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TIGS 2167 No. of Pages 12
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Trends in Genetics

Review

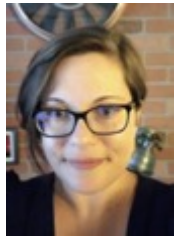
The wild side of grape genomics

Dario Cantu [1,2,*], Mélanie Massonnet [1], and Noé Cochetel [1]

With broad genetic diversity and as a source of key agronomic traits, wild grape species (*Vitis* spp.) are crucial to enhance viticulture's climatic resilience and sustainability. This review discusses how recent breakthroughs in the genome assembly and analysis of wild grape species have led to discoveries on grape evolution, from wild species' adaptation to environmental stress to grape domestication. We detail how diploid chromosome-scale genomes from wild *Vitis* spp. have enabled the identification of candidate disease-resistance and flower sex determination genes and the creation of the first *Vitis* graph-based pangenome. Finally, we explore how wild grape genomics can impact grape research and viticulture, including aspects such as data sharing, the development of functional genomics tools, and the acceleration of genetic improvement.

Our team


Rosa Figueroa-Balderas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http://cantulab.github.io/

www.grapegenomics.com

@cantulab

Funding

USDA

NSF

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UCDAVIS Chile LIFE SCIENCES INNOVATION CENT

American Vineyard Foundation

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DOLCE
Liquid Gold from Napa Valley

E&J. Gallo Winery

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Louis P. Martini Endowment in Viticulture